

Sequence	Strd Orig	ZScore	EScore	Len	Documentation
/cgn2.6/pdata/2/lna/6B_COMB.seq	US-09-103-840A-1	+	457.50	640.73	4.9e-28
/cgn2.6/pdata/2/lna/6B_COMB.seq	US-09-591-035-8	+	381.50	605.57	4.4e-26
/cgn2.6/pdata/2/lna/3B_COMB.seq	US-08-928-692-9	+	314.00	489.88	1.2e-19
/cgn2.6/pdata/2/lna/3B_COMB.seq	US-09-031-392-1	+	284.50	443.21	4.9e-17
/cgn2.6/pdata/2/lna/6A_COMB.seq	US-09-299-549-1	+	284.50	443.21	4.9e-17
/cgn2.6/pdata/2/lna/6A_COMB.seq	US-08-501-572-6	+	226.50	348.02	9.8e-12
/cgn2.6/pdata/2/lna/6A_COMB.seq	US-09-040-444-6	+	226.50	348.02	9.8e-12
/cgn2.6/pdata/2/lna/6A_COMB.seq	US-08-501-572-4	+	201.00	305.09	2.4e-09
/cgn2.6/pdata/2/lna/6A_COMB.seq	US-09-040-444-4	+	201.00	305.09	2.4e-09
/cgn2.6/pdata/2/lna/6A_COMB.seq	US-08-501-572-5	+	198.50	300.86	4.2e-09
/cgn2.6/pdata/2/lna/6A_COMB.seq	US-09-040-444-5	+	198.50	300.86	4.2e-09
/cgn2.6/pdata/2/lna/6B_COMB.seq	US-09-103-840A-2	+	195.00	197.95	0.0022
/cgn2.6/pdata/2/lna/3A_COMB.seq	US-08-676-967-5	+	167.50	246.20	4.6e-06
/cgn2.6/pdata/2/lna/3A_COMB.seq	US-08-676-974-5	+	167.50	246.20	4.6e-06
/cgn2.6/pdata/2/lna/3B_COMB.seq	US-09-098-487-5	+	167.50	246.20	4.6e-06
/cgn2.6/pdata/2/lna/3B_COMB.seq	US-08-743-637B-182	+	163.00	245.29	5.2e-06
/cgn2.6/pdata/2/lna/3B_COMB.seq	US-08-647-397-1	+	160.00	234.55	2.0e-05
/cgn2.6/pdata/2/lna/6B_COMB.seq	US-09-118-442-23	+	158.50	255.06	1.5e-06
/cgn2.6/pdata/2/lna/6B_COMB.seq	US-09-677-064-23	+	158.50	255.06	1.5e-06
/cgn2.6/pdata/2/lna/6A_COMB.seq	US-08-403-852D-6	+	155.50	228.67	4.4e-05
/cgn2.6/pdata/2/lna/6B_COMB.seq	US-08-510-646B-6	+	155.50	228.67	4.4e-05
/cgn2.6/pdata/2/lna/6B_COMB.seq	US-09-231-818-6	+	155.50	228.67	4.4e-05
/cgn2.6/pdata/2/lna/3A_COMB.seq	US-08-125-468-1	+	145.50	176.85	0.0336
/cgn2.6/pdata/2/lna/3B_COMB.seq	US-08-474-933-1	+	145.50	176.85	0.0336
/cgn2.6/pdata/2/lna/6B_COMB.seq	US-08-994-035C-4	+	144.50	193.01	0.0042
/cgn2.6/pdata/2/lna/6B_COMB.seq	US-09-103-840A-1	-	142.00	108.53	214.30
/cgn2.6/pdata/2/lna/3B_COMB.seq	US-08-494-907-13	+	140.50	207.97	0.0006
/cgn2.6/pdata/2/lna/3B_COMB.seq	PCR-US96-10986-13	+	140.50	207.97	0.0006
/cgn2.6/pdata/2/lna/6A_COMB.seq	US-08-882-046-3	+	140.50	192.66	0.0044
/cgn2.6/pdata/2/lna/3A_COMB.seq	US-08-494-907-2	+	140.50	190.63	0.0057
/cgn2.6/pdata/2/lna/3B_COMB.seq	PCR-US96-10986-2	+	140.50	190.63	0.0057
/cgn2.6/pdata/2/lna/3B_COMB.seq	US-08-494-907-4	+	140.50	188.19	0.0078
/cgn2.6/pdata/2/lna/3B_COMB.seq	PCR-US96-10986-4	+	140.50	188.19	0.0078
/cgn2.6/pdata/2/lna/3B_COMB.seq	US-08-494-907-3	+	140.50	187.76	0.0083
/cgn2.6/pdata/2/lna/3B_COMB.seq	PCR-US96-10986-3	+	140.50	187.76	0.0083
/cgn2.6/pdata/2/lna/3B_COMB.seq	US-08-753-760A-1	+	139.50	164.77	0.1579
/cgn2.6/pdata/2/lna/6B_COMB.seq	US-08-998-416-719	+	138.00	211.05	0.0004
/cgn2.6/pdata/2/lna/6B_COMB.seq	US-09-020-956-110	+	136.50	188.86	0.0072
/cgn2.6/pdata/2/lna/6B_COMB.seq	US-09-030-607-110	+	136.50	188.86	0.0072
/cgn2.6/pdata/2/lna/6B_COMB.seq	US-09-443-501A-2	+	136.50	150.72	0.0573
/cgn2.6/pdata/2/lna/6B_COMB.seq	US-09-443-501A-2	+	136.50	150.72	0.0573

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137 erLeuTyrGluAlaGlyIleThrValGlyIleLeuLeuSerTyrAlaLeu 153
   :: |||:: :: |||:: |||:: |||:: |||:: |||:: |||:: |||::
3717624CCGGTATACAGTGGCGACGCTAGCGCATCGTCGCTACCTGGTC 3717673

154 AsnTyrAlaLeuAlaGlyThrProTrpGlyTyrArgHisMetPheGlyTr 170
   :: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||::
3717674GGTACCTAGTGGCGGATCG...CAGGGCTGGCGCGATGTCGGGT 3717720

170 pAlaThrAlaProAlaValLeuGlnSerLeuSerLeuLeuPheProA 187
   |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||::
3717721GGCGCGCGCGCCAGCGTG...CTGTTGCCGTGTTGGCG... 3717762

187 LaGlyThrAspGluThrAlaThrHisLysAspLeuLeuProLeuGlnGly 203
   |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||::
3717763.....CATGCCGATACCGCGCTGATCTGCTCAAGG 3717798

204 GlyGlu.....AlaProLysLeuGlyProGlyAr 213
   :: |||:: |||:: |||:: |||:: |||:: |||:: |||::
3717799CCGGATCGCGCGCGTAGCGCTGCGCGGATCCAGCGAGGCGG 3717848

213 gProArg.TyrSerPheLeuAlaGlyThrValGlyIleLeuLeuProA 229
   |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||::
3717849ACATCGATCCGAGCTGGCGGATATGGCGCGCGCTCGACGAGCGCG 3717898

230 Gly.....ArgThrThr..... 233
   |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||::
3717899GGCGGTATCGGGAATGTCGCGCGCGGTATCTCGCGGCCAGCTGT 3717948

234 ....ValGlyLeuGlyLeuValLeuPheGlnGlnLeuThrGlyGlnProA 249
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249 snValLeuCysTyrAlaSerThrIlePheSerSerValGlyPheHisGly 265
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3717993CGATCATCTACTACAGTCCGCGATTTTCGCCGATCGGCTCGCGGC 3718042

266 GlySerSerAlaValLeuAlaSerValGlyLeuGlyAlaValLysVal 282
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3718043TATTTCGGGATGTCCTCCCGCGATGTCGCAAGTCGCGGCTTGGC 3718092

282 aAlaThrLeuThrAlaMetGlyLeuValAspArgAlaGlyArgAla 299
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3718093CGCGGTGTCCTCGCTGTTCTGTCGATCGGCTCGCGCGCGCGA 3718142

299 euLeuLeuAlaGlyCysAlaLeuMetAlaLeuSerValSerGlyIleGly 315
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3718143TCCTGTTGTCGGCATCGCGACGATG...ATCACCGCAGATGCGGCTG 3718189

316 LeuValSerPheAlaValProMetAspSerGlyProSerCysLeuAlaVa 332
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3718190ATCACCGTATTCGCCAACGACTCCGATGTCGCGCGCGCGCGA 3718222

332 lProAsnAlaThrGlyGlnThrGlyLeuPro...GlyAspSerGlyLeuL 348
   |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||::
3718223.....ACGGGCTGGTGGTGGGTTGCGCGCGCGGTCG 3718253

348 euGlnAspSerSerLeuProProIleProArgThrAsnGluAspGlnArg 364
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3718254TG..... 3718255

365 GluProIleLeuSerThrAlaLysLysThrLysProHisProArgSerGl 381
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381 yAspProSerAlaProProArgLeuAlaLeuSerSerAlaLeuProGlyP 398
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398 roProLeuProAlaArgGlyHisAlaLeuLeuArgTrpThrAlaLeuLeu 414
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415 CysLeuMetValPheValSerAlaPheSerPheGlyPheGlyProValTh 431

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3718256.....CTGTTTCATCATCGGGTTCAACTTCGATTTCGGCTCGCTGGT 3718296

431 rTrpLeuValLeuSerGluIleTyrProValGluIleArgGlyArgAlaP 448
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3718297CTGGGTGTACGCGCGGAGAGCTTCCGCTCCGCGTCCGCTCGATGGAT 3718346

448 heAlaPheCysAsnSerPheAsnTrpAlaAlaAsnLeuPheIleSerLeu 464
   :: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||::
3718347CGAGCCGATGCTCACCTCGACATGACGCGCAACGCGATCGTGGCGCC 3718396

465 SerPheLeuAspLeuIleGlyThrIleGlyLeuSerTrpThrPheLeuLe 481
   |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||::
3718397TTCGCTTCACATCATGCTGCTGCTGCGCGCGCGAGCGGTTTCGCGGT 3718446

481 uTyrGlyLeuThrAlaValLeuGlyLeuGlyPheIleTyrLeuPheValP 498
   :: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||::
3718447CTTCGCGACGTTCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3718496

498 roGluThrLysGlyGlnSerLeuAlaGluIle 508
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3718497CGGAGACCAAGCGCGCAAACTCGAGGAGATC 3718528

seq_name: /cqn2_6/ptodata/2/ina/6B_COMB.seq:US-09-591-025-8

seq_documentation_block:
; Sequence 8, Application US/09591025
; Patent No. 6303373
; GENERAL INFORMATION:
; APPLICANT: Bogan, Jonathan S.
; TITLE OF INVENTION: Method of Measuring Plasma Membrane
; TITLE OF INVENTION: Targeting of GLUT4
; FILE REFERENCE: 0399.1210-004
; CURRENT APPLICATION NUMBER: US/09/591,025
; PRIOR FILING DATE: 2000-06-09
; PRIOR FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 2592
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified GLUT4 containing myc tag sequences
US-09-591-025-8

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alignment_scores:
Quality: 381.50 Length: 486
Ratio: 1.467 Gaps: 13
Percent Similarity: 53.498 Percent Identity: 26.543

alignment_block:
US-09-652-292-2 x US-09-591-025-8 ..

Align seg 1/1 to: US-09-591-025-8 from: 1 to: 2592

56 LeuGlyAlaLeuLeuAlaSerLeuValGlyGlyPheLeuIleAspCyst 72
   :: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||::
583 GTGGCGCGCATGATTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 632

72 rGlyArgLysGlnAlaIleLeuGlySerAsnLeuValLeuAlaGlyS 89
   |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||::
633 TGGAGGAAAGGCGGCATGCTGTCACAAATGCTCTGCGCGGTCTGGGG 682

89 erLeuThrLeuGlyLeuAlaGlySerLeuAla.....TrpLeuVal 102
   :: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||::
683 GCAGCCTCATGGGCTGGCGCAACGCTGCTGCTCTATGAATGCTCATC 732

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[illegible]

seq\_documentation\_block:

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seq_documentation_block:
; Sequence 9, Application US/08928692
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Patent No. 5958727  
GENERAL INFORMATION:

;  
;  
;  
;

APPLICANT: Lamsa, Michael

; APPLICANT: Hansen, Kim

**TITLE OF INVENTION:** Methods for M

NUMBER OF SEQUENCES: 80

CORRESPONDENCE ADDRESS

ADDRESSEE: NO. 5958727o NO. 5958727disk of NO. 5958727th America, Inc.

STREET: 405 Lexington Avenue

CITY: New York  
STATE: NY

COUNTRY: USA

; ZIP: 10174

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM compatible

COMPUTER: IBM COMPACID  
OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/

FILING DATE: 12-SEPT-85  
CLASSIFICATION: A35

CLASSIFICATION: 433  
ATTORNEY/AGENT INFORMATION:

NAME: Lambiris, Elias J

REGISTRATION NUMBER: 33,728

REFERENCE/DOCKET NUMBER: 49

TELECOMMUNICATION INFORMATION  
TELEPHONE: 312-867-0123

TELEPHONE: 212 607 0123  
TELEFAX: 212-878-9655

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

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; LENGTH: 3000 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-928-692-9

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alignment_scores:
  Quality: 314.00      Length: 591
  Ratio: 1.150         Gaps: 18
  Percent Similarity: 46.193  Percent Identity: 23.181

alignment_block:
US-09-652-292-2 x US-08-928-692-9 ..

Align seg 1/1 to: US-08-928-692-9 from: 1 to: 3000

      2  GlyHisSerProValLeuProLeuCysAlaSerValSerLeuLeuG 18
      |||||  |||  |||  |||||  |||  |||||  |||  |||||  |||
    557  GGTACTCGTACTCGTACTGATCTACTGTTG.....TTTATCAACAACCTTGG 600

      18  lyGlyLeuThrPheGlyTyrGluLeuAlaValIleSerGlyAlaLeuLeu 34
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
    601  GGCACTTCAATTCCGATATCATTTG...GTATTACGCGAGCTTGGTCT 647

      35  ProLeuGlnLeuAspPheGlyLeuSer..... 43
      ||||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:
    648  ATGCTGGAGGC...TTCAATACATCGGCTGACATATATTATGATAGCC 693

      43  ..... 43

    694  TGAGCTCAATGCCCCCGAGCGCGTGATAACTTGGAGCGGAAAGCATCC 743

    44  .....CysLeu.....Glu 46
      ||||:  ||||:  ||||:  ||||:  ||||:  ||||:  ||||:  ||||:
    744  ATTCGACAACAACACGGGTCTCCCGCAATGCATACCTATGAACCCATCC 793

    47  GlnGluPheLeuValGlySerLeu...LeuLeuGlyAlaLeuLeuAlaIse 62
      |||  |||||  |||||  ||||:  ||||:  ||||:  ||||:  ||||:
    794  CAATTGGCGCTGTCTCTCTATATACACCTCTGGGGCTTGGCTTAGGGGC 843

    62  rLeuValGlyGlyPheLeuIleAspCysTyrGlyArgLysGlnAlaIleL 79
      ||||:  ||||:  |||  |||  |||  |||  |||  |||  |||  |||
    844  TCTCTGCGAGGTCACGTTTCCACCAACGATGGCGCTTGTTCACATGC 893

    79  euGlySerAsnLeuValLeuLeuAlaGlySerLeuThrLeuGlyLeuAla 95
      ||||:  ||||:  ||||:  ||||:  ||||:  ||||:  ||||:  ||||:
    894  GAGCGACCACTCTCTCTATCTAGGCCCTATAGCAGAAACATTTGCG 943

    96  GlySerLeuAlaTrpLeuValLeuGlyArgAlaValValGlyPheAlaII 112
      ||||:  |||  |||  |||||  |||  |||  |||  |||  |||  |||
    944  CCCAGTATACCGTATTGAGTATGGGTAGGCTTTATCTGGTGTGTGTGC 993

    112  eSerLeuSerSerMetAlaCysCysIleThrValSerGluLeuValGlyP 129
      ::|  |||  ||||:  ||||:  ||||:  ||||:  ||||:  ||||:
    994  GGGCGCTTCTATCTGCTGGTCCGATATATCTCTGAGTATGCTCTCCT 1043

    129  roArgGlnArgGlyValLeuValSerLeuTyrGluAlaGlyIleThrVal 145
      ||  ||  ||||:  ||||:  ||||:  ||||:  ||||:  ||||:
    1044  CTAGTGTAAAGGTCTTTTTCGGCGCTTTTACGGAATCATGACATAATGTC 1093

    146  GlyIleLeuLeuSerTyrAlaLeuAsnTyrAlaLeuAlaGlyThrProTr 162
      ||||:  ||||:  ||||:  ||||:  ||||:  ||||:  ||||:  ||||:
    1094  GGTATTCTGTGACACAGTCCCTTGGTTACTTCTTGGTAAAGGAAGTAT 1143

    162  pGlyTrpArgHisMetPheGlyTrpAlaThrAlaProAlaValLeuGlnS 179
      |||||  |||||  ||||:  |||  |||  |||  |||  |||  |||
    1144  G...TGAGAGATTATATTGCAATTCTGGCGGATCGGATGCTTGACC 1190

    179  erLeuSerLeuPheLeuProAlaGlyThrAspGluThrAlaThrHis 195
      ||||:  ||||:  ||||:  ||||:  ||||:  ||||:  ||||:  ||||:
    1191  TTCTGGGCTCTTCTTAGTCCCAAGAACGCCCATCTGGCTTCGACATCAC 1240
  
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455 AsnTrpAlaAlaAsnLeuPheIleSerLeuSerPhe.....LeuAs 468
||||| ||||| :||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1859 AACTGGATTGCCACGCTTCATCGTGGCAGAAATTTTCCGATGTATAACGA 1908
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
468 PLeuIleGlyThrIleGly...LeuSerTrpThrPheLeuLeuTyTyrGlyL 484
||||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1909 TTTGTTGGCGGCAGGCAAGATCTACTGGATCTTGCA.....GCGA 1952
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
484 euThrAlaValLeuGlyLeuGlyPheIleTyTyrPheValProGluThr 500
||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1953 TGGCGTGCTCTCTCGGA...AGTTTCATCTACTGGTGGGTGCCGGAGACC 1999
||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
501 LysGlyGlnSerLeuAlaGlu 507
||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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[illegible]

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1  APPLICANT: Tartaglia, Louis A.
2  APPLICANT: Weng, Xun
3  TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
4  TITLE OF INVENTION: GLUTEX AND USES THEREOF
5  NUMBER OF SEQUENCES: 10
6  CORRESPONDENCE ADDRESS:
7  ADDRESSEE: Fish & Richardson P.C.
8  STREET: 225 Franklin Street
9  CITY: Boston
10 STATE: MA
11 COUNTRY: USA
12 ZIP: 02110-2804
13 COMPUTER READABLE FORM:
14 MEDIUM TYPE: Diskette
15 COMPUTER: IBM Compatible
16 OPERATING SYSTEM: Windows95
17 SOFTWARE: FASTSEQ for Windows Version 2.0
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/09/299,549
20 FILING DATE: 26-APR-1999
21 PRIORITY DATA:
22 APPLICATION NUMBER: 09/031,392
23 FILING DATE: 26-FEB-1998
24 ATTORNEY/AGENT INFORMATION:
25 NAME: Meikiejohn, Ph.D., Anita L.
26 REGISTRATION NUMBER: 35,283
27 REFERENCE/DOCKET NUMBER: 07334/072002
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE: 617/542-5070
30 TELEFAX: 617/542-8906
31 TELEX: 200154
32 INFORMATION FOR SEQ ID NO: 1:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH: 2343 base pairs
35 TYPE: nucleic acid
36 STRANDEDNESS: single
37 TOPOLOGY: linear
38 MOLECULE TYPE: gDNA
39 FEATURE:
40 NAME/KEY: Coding Sequence
41 LOCATION: 73...1761
42 US-09-299-549-1
43
44 alignment_scores:
45 Quality: 284.50 Length: 581
46 Ratio: 1.078 Gaps: 16
47 Percent Similarity: 45.439 Percent Identity: 20.138
48
49 alignment_block:
50 US-09-652-292-2 x US-09-299-549-1 ..
51
52 Align seg 1/1 to: US-09-299-549-1 from: 1 to: 2343
53
54 10 LeuCysAlaSerValSerLeuLeuGlyGlyLeuThrPhe.....GlyTy 24
55 ||| |||||:|:|:|:| ||| |||||
56 241 CTCGCGGCCTCCCTCGCGGCGCCCTCGGCTCTCTCTCTACGGCTA 290
57 ||| |||||:|:|:|:| ||| |||||
58 24 rGluLeuAlaValIleSerGly..... 31
59 ||| |||||:|:|:|:| ||| |||||
60 291 CAACCTGTCTGGTGGTGAATGCCCCACCCGATCAAGAGCGCTTTTACA 340
61 ||| |||||:|:|:|:| ||| |||||
62 32 .....AlaLeuLeuProLeuGlnLeu 38
63 ||| |||||:|:|:|:| ||| |||||
64 341 ATGAGTCATGGAAGAAGGATGACGTCCTCAATAGACCCAGACTCTG 390
65 ||| |||||:|:|:|:| ||| |||||
66 39 AspPheGlyLeuSerCysLeuGluGlnGluPheLeuValGlySerLeu 55
67 ||| |||||:|:|:|:| ||| |||||
68 391 ACTCTGCTGTGCTGTGACTGTGTCTCCATATTCGCCATCGGTGGA...CT 437
69 ||| |||||:|:|:|:| ||| |||||
70 55 uLeuGlyAlaLeuLeuAlaSerLeuValGlyGlyPheLeuIleAspCys 72
71 ||| |||||:|:|:|:| ||| |||||
72 438 TGTGGGACGCTTAATTGTGACATGATTGGAAAGGTTCTT..... 477

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501,572
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Toohey, Kimberlin M
REGISTRATION NUMBER: 35,391
REFERENCE/DOCKET NUMBER: 02481.1453-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)408-4000
TELEFAX: (202)408-4400
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1896 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-501-572-6

alignment_scores:
Quality: 226.50          Length: 570
Ratio: 0.956            Gaps: 22
Percent Similarity: 41.579    Percent Identity: 20.175

alignment_block:
US-09-652-292-2 x US-08-501-572-6 ..

Align seg 1/1 to: US-08-501-572-6 from: 1 to: 1896

39 AspPheGlyLeuSerCysLeuGlutIn.....GluPheLeuValGI 52
   ::|||::||| ||| ::::::::::::
556 GAGTTTAACTGGTATGTGCCAACTCCTCGATGTTGGACCTATTCCAGTC 605
      ySerLeuLeuGlyAlaLeuLeuLaSerLeuValGLyGlyPheLeuI 69
      :|||::: ::||| :::::::::::||||: |:|||:::
606 ATCAGTGAAATGAGGATTCCTTATTGGCTCTTAGAGTATCGGCCTACATAG 655
      leAspCysTyRGlyArgLysGlnAlaileLeuGlySerAsnLeuValLeu 85
      ||| ::|||::|||::| ::::::|::| ::| ::|:::
656 CAGACAGGTTTGGCCGTAAGCTCTGCCTCACTACAGTCGCTCATATAAT 705
      LeuAlaGlySerLeuThrLeuGlyLeuAlaGLySerLeuLeuTrpLeuVa 102
      |||::|::|::|::| ::::::|::|::| ::|::|::|::|::|::|
706 GCTGCAGCTGGAGTTCTCATGGCCAFTTCCCACAACCTATACGTGGATGTT 755
      lleuGlyArgAlaValAlcLyPheAlaileSerLeuSerMetAlac 119
      ::| ::| ::| ::|::|::|::|::| ::|::|::|::|::|::|
756 AATTTTTTCGCTTAATCAAAGGACTGGTCAGCAAAACAGCGCTGGTTAATAG 805
      yScysteIeTyrValSerGluLeuValGLyProArgGlnArgGlyValLeu 135
      ||| ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
806 GTACATCTCTGATTACAGAATTTGTGGGGGAGATATCGGAACAACATG 855
      ValSerLeuTyRgLUAlaGlyleThrValGlyleLeuLeuSerTyraL 152
      ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|
856 GGGATTTTTACCAGTTGCCTATACAGTGGCTGGCTCTGGTGCTAGCTGG 905
      aleuAsnTyRaLeuAlaGlyThrProTrpGlyTrpArghis..... 166
      ::| ::|::|::|::|::|::|::|::|::|::|::|::|::|::|
906' GGTCGCTTACGCACATT.....CCTCACTGGAGGTGGTTGCAGTTCACAG 949
      MetPheGlyTrpAla..... 171
      | ..... 171
950 TTGCTCTGCCCAACTTCCTTCCTTGTGCTATTACTGGTGCACTACCTGAG 999
      ThrAlaProAlaValLeug 178
      ::| ::|::|::|::|::|::|::|::|::|::|::|::|::|::|
171 ..... 171
1000 TCTCCAGGTGGCTGATCTCCCAAGAATAAGAACTCGNAGCCATGACAAT 1049
172 .....ThralaProAlaValLeug 178
      ::| ::|::|::|::|::|::|::|::|::|::|::|::|::|::|

```



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463 erLeuSerPheLeuAspLeuIleGlyThrIleGlyLeuSerTrpThrPhe 479
1558 ....TCAATGTGTGACATTTGGTGGCATCATC.....ACGCCATTTC 1593
480 LeuLeuTyrGlyLeuThr..... 485
1594 CTGGCTACCGCTCACTAACATCTGGCTTGGCTGAGTCCCGCTGATGGTTTT 1643
486 AlaValLeuGlyLeu.....GlyPheIleTyrLeuPheValProGluT 500
1644 CGCGCTACTTGGCTGGTGGCTGGAGGTGCTGCTGTTGCTTCCAGAA 1693
500 hrLysGlyGlnSerLeuAlaGluIleAspGlnGlnPheGlnLysArgArg 516
1694 CTAAGGGAAGCTTTGCCCTGAGACCATCGAGGAGCCGAGAAATATGCAA 1743
517 PheThrLeuSerPheGlyHisArgGlnAsnSerThrGlyIleProTyrSe 533
1744 .....AGACCAAGAAATAAAGAAAGATGATTTACCT 1778
533 rArgIleGlu 536
1779 CCAAGTTTCA 1788

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seq\_name: /cgn2\_6/ptodata/2/1na/6A\_COMB.seq:US-09-040-444-6

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seq_documentation_block:
; Sequence 6, Application US/09040444
; Patent No. 6063766
; GENERAL INFORMATION:
; APPLICANT: Koepsell, Hermann
; APPLICANT: Grundeman, Dirk
; APPLICANT: Gorboulev, Valentin
; TITLE OF INVENTION: Transport protein which effects the
; TITLE OF INVENTION: Transport of cationic xenobiotics and/or pharmaceuticals,
; TITLE OF INVENTION: DNA sequences encoding it and their use.
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner, L.L.P.
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/040.444
; FILING DATE: March 18, 1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: O'Connor, Steven P
; REGISTRATION NUMBER: 41,225
; REFERENCE/DOCKET NUMBER: 2481.1453-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)408-4000
; TELEFAX: (202)408-4400
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1896 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-040-444-6

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alignment\_scores: Quality: 226.50 Length: 570

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Ratio: 0.956 Caps: 22
Percent Similarity: 41.579 Percent Identity: 20.175
alignment_block:
US-09-652-292-2 x US-09-040-444-6
Align seg 1/1 to: US-09-040-444-6 from: 1 to: 1896
39 AspPheGlyLeuSerCysLeuGluGln.....GluPheLeuVal1 52
556 GAGTTTAACTGCTATGTCACCAACTCCTGGATGTTGGACCTATTCCAGTC 605
52 ySerLeuLeuGlyAlaLeuLeuAlaSerLeuValGlyGlyPheLeu1 69
606 ATCAGTGAATAGGATGCTTTATTGGCTCTATGATATCGCTACATAG 655
69 LeAspCysTyrGlyArgLysGlnAlaIleLeuGlySerAsnLeuValLeu 85
656 CAGACAGGTTTGGCGTAAAGCTCTGCCTCCTAACTACAGTCTCTAAT 705
86 LeuAlaGlySerLeuThrLeuGlyLeuAlaGlySerLeuAlaTrpLeuVa 102
706 GCTGCAGCTGGAGTCTCATGGCCATTCCCAACCTATACCTGGATGTT 755
102 lLeuGlyArgAlaValValGlyPheAlaIleSerLeuSerSerMetAlaC 119
756 AATTTTTCCTTAATCCCAAGGACTGGTCAGCAAGCAGGCTGGTTAATAG 805
119 yScysIleTyrValSerGluLeuValGlyProArgGlnArgGlyValLeu 135
806 GCTACATCTGATTACAGAAATTTGTTGGGGGAGATATCGGAGACAGTG 855
136 ValSerLeuTyrGluAlaGlyIleThrValGlyIleLeuLeuSerTyrAl 152
856 GGGATTTTATCAAGTTCCCTATACAGTTGGCTCCTGGTGTCTAGCTGG 905
152 aLeuAsnTyrAlaLeuAlaGlyThrProTyrGlyTrpArgHis..... 166
906 GGTGGCTTACGCATTT.....CCTCACTGGAGTGGTTGCAGTTCCACAG 949
167 .....MetPheGlyTrpAla..... 171
950 TTGCTCTGCCCAACTTCTTCTTCTGCTCTATTACTGGTGGCATACCTGAG 999
171 ..... 171
1000 TCTCCAGGTGCTGATCTCCCAAGATAAGAAATGCTGAAGCCATGAGAAT 1049
172 .....ThrAlaProAlaValLeuG 178
1050 CATTAAAGCACATCGCAAGAAAAATGGAANAATCTCTACCCGCTCCCTTC 1099
178 lSerLeuSerLeuLeuPheLeuProAlaGlyThrAspGluThrAlaThr 194
1100 ACGGCTGAGACTT.....GAAGAGGAAACT 1125
195 HisLysAspLeuIleProLeuGlnGlyGluAlaProLysLeuGlyPr 211
1126 GGCAAGAAATTCAGCCCT..... 1143
211 OGlyArgProArgTyrSerPheLeuAspLeuPheArgAlaArgAspAsnM 228
1144 .....TCATTTCTTGACTTGGTCAGAACT...CCTCAGA 1174
228 eArgGlyArgThrThrValGlyLeu..... 236
1175 TAAGGAACATCTATGATATTGATGTACAACTGGTTTCAGAGCTCTGTG 1224
237 .....GlyLeuValLeuPheGlnGlnLeuThrGlyGlnProAsnVa 250
1225 CTCTACAGGCGCTCATCATGACATGGCGCTTGCAGGTGAC...AATAT 1271
250 lLeuCysTyrAlaSerThrIlePheSerSerValGlyPheHisGlyLys 267

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1272 C.....TACCTGATTCTTCTACTCTGCCCTG..... 1299
267 erSerAlaValLeuAlaSerValGlyLeuGlyAlaValLysValAlaAla 283
1300 .....GTTGAATCCAGCT 1314
284 ThrLeuThrAlaMetGlyLeuValAspArgAlaGlyArgAlaLeuLeu 300
1315 GCCTTCATGATCATCTCTCATTCGACCGCATCGGACCGCTTACCCCTG 1364
300 uLeuAlaGlyCysAlaLeuMetAlaLeuSerValSerGlyIleGlyLeuV 317
1365 GGCTGCATCA..... 1374
317 alSerPheAlaValProMetAspSerGlyProSerCysLeuAlaValPro 333
1375 .....AATATGGTTCGAGGCGCAGCTGTCTGCC..... 1404
334 AsnAlaThrGlyGlnThrGlyLeuProGlyAspSerGlyLeuGlnAs 350
1405 .....TCAGTCTTTTATACCTGTGTAT..... 1425
350 pSerSerLeuProProIleProArgThrAsnGluAspGlnArgGluProI 367
1425 ..... 1425
367 leLeuSerThrAlaLysLysThrLysProHisProArgSerGlyAspPro 383
1425 ..... 1425
384 SerAlaProProArgLeuAlaLeuSerSerAlaLeuProGlyProProLe 400
1425 ..... 1425
400 uproAlaArgGlyHisAlaLeuLeuArgTrpThrAlaLeuLeu.....C 415
1426 .....CTACAATGGCTAAATAATTATTATCTCAT 1453
415 ysLeu.....MetValPheValSerAlaPheSerPheGlyPheGlyPro 429
1454 GCTTGGAGNATGGGATCACAATGGCTATGAG..... 1488
430 ValThrTrpLeuValLeuSerGluIleTrpProValGluIleArgGlyAr 446
1489 ATAGTCTGCCTGGTCAATGCTGAGCTACCCCATTCATTAGGAATCT 1538
446 gAlaPheAlaPheCysAsnSerPheAsnTrpAlaAlaAsnLeuPheIleS 463
1539 TGGCGTCCACATCTGTTC..... 1557
463 erLeuSerPheLeuAspLeuIleGlyThrIleGlyLeuSerTrpThrPhe 479
1558 .....TCAATGTGTGACATTGGTGGCATCATC.....ACGCCATTC 1593
480 LeuLeuTyroGlyLeuThr..... 485
1594 CTGGTCTACCGCTCACTAATCACTGGCTGAGCTCCGCTGATGTTT 1643
486 .AlaValLeuGlyLeu.....GlyPheIleTyroLeuPheValProGluT 500
1644 CGCGGTACTTGGCTGGTGGTGGAGGCTGTGTGTGTGTTCAGAAA 1693
500 hrlYsglyGlnSerLeuAlaGluIleAspGlnGlnPheGlnLysArg 516
1694 CTAAGGGAAGACCTTGTGCTGAGACCATCGAGGAAGCGGAAATATGCAA 1743
517 PheThrLeuSerPheGlyHisArgGlnAsnSerThrGlyIleProTyroSe 533
1744 .....AGACCAAGAAAAAATATAGAAAGATGATTACCT 1778
533 rArgIleGlu 536
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1779 CCAAGTTTCAG 1788

seq\_name: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:US-08-501-572-4

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seq_documentation_block:
; Sequence 4, Application US/08501572
; Patent No. 6063623
; GENERAL INFORMATION:
; APPLICANT: Koepsell, Hermann
; APPLICANT: Grundeman, Dirk
; APPLICANT: Gorboulev, Valentin
; TITLE OF INVENTION: Transport protein which effects the
; TITLE OF INVENTION: Transport of cationic xenobiotics and/or pharmaceuticals,
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/501,572
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Toohy, Kimberlin M
; REGISTRATION NUMBER: 35,391
; REFERENCE/DOCKET NUMBER: 02481.1453-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)408-4000
; TELEFAX: (202)408-4400
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1882 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-501-572-4
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## alignment\_scores:

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Quality: 201.00 Length: 546
Ratio: 0.824 Gaps: 24
Percent Similarity: 44.689 Percent Identity: 23.260
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## alignment\_block:

US-09-652-292-2 x US-08-501-572-4

Align seg 1/1 to: US-08-501-572-4 from: 1 to: 1882

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37 GlnLeuAspPheGlyLeuSerCysLeuGluGlnGluPheLeuValGlySe 53
.....|.....|.....|.....|.....|.....|
479 AAAGTGGACCTTTTCAGTCTCTGTGTGGAAC..... 508
53 rLeuLeuLeuGlyAlaLeuLeuAlaSerLeuValGlyGlyPheLeuIleA 70
.....|.....|.....|.....|.....|.....|
509 .....TTGGGCTTCTCTGGGCTCCCTGTTGGGTTCATATTGCAG 551
70 spCystyrGlyArgLysGlnAlaIleLeuGlySerAsnLeuValLeuLeu 86
||.....|.....|.....|.....|.....|.....|
552 ACAGGTTTGGCGTAAGCTCTCTCTTGTGTGACCCAGCTGTCATCT 601
87 AlaGlySerLeuThrLeuGlyLeuAlaGlySerLeuAlaTrpLeuValLe 103
.....|.....|.....|.....|.....|.....|
602 GTGTCCGGTGTGCTAACACAGCGGTGCCCCCAGACTATACATCATGTTGCT 651
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; ATTORNEY/AGENT INFORMATION:
; NAME: O' Connor, Steven P
; REGISTRATION NUMBER: 41,225
; REFERENCE/DOCKET NUMBER: 2481.1453-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)408-4000
; TELEFAX: (202)408-4400
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1882 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-040-444-4

alignment_scores:
    Quality:      201.00      Length:      546
    Ratio:        0.824       Gaps:       24
    Percent Similarity: 44.689   Percent Identity: 23.260

alignment_block:
US-09-652-292-2 x US-09-040-444-4 ..

Align seg 1/1 to: US-09-040-444-4 from: 1 to: 1882

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37 GlLeuAspPheGlyLeuSerCysLeuGluGlnGluPheLeuValGlySe 53
   : :::::::::::::::::::: |||||:::
479 AAGTGACCCTTTTTCAGTCTGTGTGAAC..... 508
53 rLeuLeuGlyAlaLeuLeuAlaSerLeuValGlyGlyPheLeuIleA 70
   : ||||| : ::|||:|||||:||||| : :::::
509 .....TTGGGCTTCTCTCGGCTCCCTGGTTGGGTTGCATGTGCAG 551
70 spcysTyrgLyArgLysGlnAlaIleLeuGlySerAsnLeuValLeu 86
   : || : |||||:||||| : ::||| : ::|||:
552 ACAGGTTGGGCCCTAAAGCTCTGTCTCTGTGTGACCAAGCTGGTCA 651
87 AlaGlySerLeuThrLeuGlyLeuAlaGlySerLeuAlaTrpLeuVal 103
   : :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
602 GTGTCCGGGTGCTAACACGGGTGGCCCCAGACTATATCATCTGTTCT 651
103 uGlyArgAlaValValGlyPheAlaIleSerLeuSerMetMetAlaCy 120
   : ||| :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
652 CTTTCGCCCTGCTGCAGGGCATGTCAGCAAGGCAAGCTGGTGTGCG 701
120 ysIleTyrValSerGlulLeuValGlyProArgGlnArgGlyValLe 136
   : :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
702 ATACCTTTGATCACACAGTTTGTGGCTCTGGCTACAGGAAGAACGG 751
137 SerLeuTyrgLuAlaGlylleThrValGlylleLeuLeuSerTyraLe 153
   : |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
752 ATTTTGTACCAAGATGGCCTTCACAGTGGGGCTAGTGGGGCTTGC 801
153 uAsnTyrrAlaLeuAlaGlyThrpTroTgLYTpArgHisMetPhegly 170
   : :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
802 GGCCATATGCCATT.....CCAGACTGGCGCTGGCTCCAGCTAGCT... 841
170 rpAlaThrAlaProAlaValLeuGlnSerLeuSerLeuLeuPheLeuPr 186
   : :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
842 ..GTGTCCCTCCCTACCTTCTCTCTCTGTGTATTACTGGTTGTGCC 889
187 AlaGly.....ThraspGluThrAlaLath 194
   : ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
890 GAATCCCCCGGTGGCTGTGTGCCAGAGAAGAACCAACGCGACTGTGTA 939
194 rHisLysAspLeuIleProLeuGlnGlyGlyGluAlaPro..... 207
   : :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
940 GATAATGGAGCAAATTGCACAGAAGACGGGAAGGTGCCTCTCTGTGAC 989
208 .....LysLeuGlyProGly 212
   : ||| :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

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1341 ..... 1341  
331 laValProAsnAlaThrGlyClnThrGlyLeuProGlyAspSerGlyLeu 347  
1342 ..... 1342  
348 LeuGlnAspSerSerLeuProProIleProArgThrAsnGluAspGlnAr 364  
1347 ..... 1347  
364 gGluProIleLeuSerThrAlaLysThrLysProHisProArgSerG 381  
1347 ..... 1347  
381 lyAspProSerAlaProProArgLeuAlaLeuSerSerAlaLeuProGly 397  
1347 ..... 1347  
398 ProProLeuProAlaArgGlyHisAlaLeuLeuArgTrpThrAlaLeuLe 414  
1348 ..... 1348  
414 uCysLeuMetValPheValSerAlaPheSerPheGlyPheProValT 431  
1368 AATCATGTGTGTGGCGGAATGGGAATCACCATTGCAATAAATGATCT 1417  
431 hrTrpLeuValLeuSerGluIleTyProValGluIleArgGlyArgAla 447  
1418 GC...CTGTGAATGCTGAGCTGTACCCACATTCGTCAGGAACCTCAGA 1464  
448 PheAlaPheCysAsnSerPheAsnTrpAlaAlaAsnLeu.....Ph 461  
1465 GTGATGGTGTCTCTCTCTGTGTGACATAGTGGGATAATCAACCCCTT 1514  
461 eileSerLeuSerPheLeuAspLeuIleGlyThrIleGlyLeuSerTrp 478  
1515 CATAGCTTCAGGCTGAGGAGGTC.....TGGC 1543  
478 hrPheLeuLeuTyroGlyLeuThrAlaValLeuGlyLeu.....GlyPhe 492  
1544 AAGCCTTCCCTCATTTTGTGGGTGTGGGCTGCTTGGCGCGGA 1593  
493 IleTyroLeuPheValProGluThrLysGlyClnSerLeuAlaGlu 507  
1594 GTGACGCTACTTCTCCAGAGACCAAGGGGACGCTTGGCAAG 1638

seq\_name: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:us-09-040-444-5

seq\_documentation\_block:  
: Sequence 5, Application US/09040444  
: Patent No. 6063766  
: GENERAL INFORMATION:  
: APPLICANT: Koepsell, Hermann  
: APPLICANT: Grundeman, Dirk  
: APPLICANT: Gorboulev, Valentin  
: TITLE OF INVENTION: Transport protein Which Effects The  
: TITLE OF INVENTION: Transport Of Cationic xenobiotics and/or Pharmaceuticals,  
: TITLE OF INVENTION: DNA Sequences Encoding It And Their Use.  
: NUMBER OF SEQUENCES: 6  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner, L.L.P.  
: STREET: 1300 I Street, N.W., Suite 700  
: CITY: Washington  
: STATE: D.C.  
: COUNTRY: USA  
: ZIP: 20005-3315  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: PatentIn Release #1.0, Version #1.30  
: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/09/040,444  
: FILING DATE: March 18, 1998  
: CLASSIFICATION:  
: ATTORNEY/AGENT INFORMATION:  
: NAME: O'Connor, Steven P  
: REGISTRATION NUMBER: 41,225  
: REFERENCE/DOCKET NUMBER: 2481.1453-01  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (202)408-4000  
: TELEFAX: (202)408-4400  
: INFORMATION FOR SEQ ID NO: 5:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 1885 base pairs  
: TYPE: nucleic acid  
: STRANDEDNESS: single  
: TOPOLOGY: linear  
: MOLECULE TYPE: DNA (genomic)  
: US-09-040-444-5

alignment\_scores:  
Quality: 198.50 Length: 515  
Ratio: 0.906 Gaps: 17  
Percent Similarity: 42.524 Percent Identity: 20.971  
alignment\_block:  
US-09-652-292-2 x US-09-040-444-5 ..  
Align seg 1/1 to: US-09-040-444-5 from: 1 to: 1885

37 GlnLeuAspPheGlyLeuSerCysLeuGluGlnGluPheLeuValGlySe 53  
511 AAGCTGGACCTCTTTTCAGTCTCTTTGAATGGGGCTTCTTCTTGGCTC 560  
53 rLeuLeuLeuGlyAlaLeuAlaSerLeuValGlyGlyPheLeuLea 70  
561 TCTCGGTGTT.....GGCTACTTTGCGAG 583  
70 spCysTyroGlyArgGlyGlnAlaIleLeuGlySerAsnLeuValLeuLeu 86  
584 ACAGGTTTGGCGGTAAAGCTGTCTCTCTGGGAACCTGTCTGTCAACGCG 633  
87 AlaGlySerLeuThrLeuGlyLeuAlaGlySerLeuAlaTrpLeuValLe 103  
634 GTGTGGGGGTCTCATGGCTTCTGCGCCCACTACATGTCCATGCTGCT 683  
103 uGlyArgAlaValValGlyPheAlaIleSerLeuSerSerMetAlaCysC 120  
684 CTTCGCGCTGCTGCAGGGCTGGTCAGCAAGGCAACTGGATGCTGGCT 733  
120 ysIleTyroValSerGluLeuValGlyProArgGlnArgGlyValLeuVal 136  
734 ACACCTTAATCAGAAATTTGTGGCTGGGCTCCAGAAAGACGGTGGCG 783  
137 SerLeuTyroGluAlaGlyIleThrValGlyIleLeuLeuSerTyroAlaLe 153  
784 ATCATGTACAGATGGCTTCAAGCTGGGCTGGGCTGGGCTTACCGGCT 833  
153 uAsnTyroAlaLeuAlaGlyThrProTrpGlyTyroArgHis..... 166  
834 GGCCTAGCCCTG.....CCTCAGTGGCGCTGGCTGCAGCTGGCAGTCT 877  
167 .....MetPheGlyTrpAlaThrAlaProAla 175  
878 CCCTGCCACCTTCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 915  
176 ValLeuGlnSerLeuSerLeuLeuPheLeuProAlaGlyThrAspGluTh 192  
916 GTCCCGGAGTCCCTCGTGGCTGTTATCACAAGAAAGAAACACTGAAGC 965  
192 rAlaThrHisLysAspLeuIleProLeuGlnGlyGlyGluAlaPro.... 207  
966 AATAAAGATAATGGACCATCGTCAAAAGAAATGGGAAGTTGCCTCTCTG 1015

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208 .....LysLeuGly 210
1016 CTGATTAAAGATGCTTTCCCTCGAAGAGGATGTCACCGAAAAGCTGAGC 1065
211 ProGlyArgProArgTyrSerPheLeuAspLeuPheArgAlaArgAspAs 227
1066 CCT.....TCATTTCGACACCTGTTCCGACG....CCGGC 1097
227 nMetArgGlyArgThrThrValGlyLeuGlyLeu.....V 239
1098 CCTGAGGAGCGCACCTTCATCTGCTGATCTGCTGTTTCACGGACTCG 1147
239 aLeuPheGlnGlnLeu.....ThrGlyGlnProAsnValLeuCys 252
1148 TGCTCTATCAGGGGCTCATCTCTGCACATGGCGCCACCGAGGACCTC 1197
253 TyrAlaSerThrIlePheSerSerValGlyPheHisGlyGlySerSerAl 269
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269 aValLeuAlaSerValGlyLeuGlyAlaValLysValAlaAlaThrLeuT 286
1225 .....GTGGAATCCCGGGGCTTCA 1246
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1247 TAGCCCTCATCACCATTTGACCGCGTGGCGCATCTACCCCATGGCGGTG 1296
298 AlaLeuLeuAlaGlyCysAlaLeuMetAlaLeuSerValSerGlyI 314
1297 TCNAATTTGTTGGCGGGCAGCTCCCTCGTCATTTTATCTCA.... 1341
314 eGlyLeuValSerPheAlaValProMetAspSerGlyProSerCysLeuA 331
1341 ..... 1341
331 laValProAsnAlaThrGlyGlnThrGlyLeuProGlyAspSerGlyLeu 347
1342 .....CCTGAC..... 1347
348 LeuGlnAspSerSerLeuProProIleProArgThrAsnGluAspGlnAr 364
1347 ..... 1347
364 gGluProIleLeuSerThrAlaLysLysThrLysProHisProArgSerG 381
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381 lyAspProSerAlaProProArgLeuAlaLeuSerSerAlaLeuProGly 397
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398 ProProLeuProAlaArgGlyHisAlaLeuLeuArgTrpThrAlaLeuLe 414
1348 .....CTGCACCTGGTTAAACATCAT 1367
414 uCysLeuMetValPheValSerAlaPheSerPheGlyPheGlyProValT 431
1368 AATCATGTGTGTGGCGGAATGGAAATCACCATTGCAATACAANTGATCT 1417
431 hrTrpLeuValLeuSerGluIleTyrProValGluIleArgGlyArgAla 447
1418 GC...CTGGTGAATGTGAGCTGTACCCACATTCGTCAGGAACCTCAGA 1464
448 PheAlaPheCysAsnSerPheAsnTrpAlaAlaAsnLeu.....Ph 461
1465 GTGATGGTGTGTTCCCTGCTGTGACATAGGTGGGATAATCACCCTT 1514
461 eileSerLeuSerPheLeuAspLeuIleGlyThrIleGlyLeuSerTrpT 478
1515 CATAGTCTTCAGGCTGAGGAGGTC.....TGSC 1543
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478 hrPheLeuLeuTyrGlyLeuThrAlaValLeuGlyLeu.....GlyPhe 492
1544 AGCCTTGCCCTCATTTTGGCGGTGTTGGGCTGCTTCCCGCGGA 1593
493 ileTyrLeuPheValProGluThrLysGlyGlnSerLeuAlaGlu 507
1594 GTGACGCTACTTCTCCAGACACCAAGGGGACGCTTTCACAGAG 1638
seq_name: /cgn2_6/ptodata/2/lna/6B_COMB.seq:US-09-103-840A-2
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seq_documentation_block:
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103.840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
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alignment_scores:
  Quality: 195.00      Length: 517
  Ratio: 0.786        Gaps: 21
  Percent Similarity: 47.969      Percent Identity: 22.824

alignment_block:
US-09-652-292-2 x US-09-103-840A-2/rev ..

Align seg 1/1 to reverse of: US-09-103-840A-2 from: 1 to: 4403765

12 AlaSerValSerLeuLeuGlyGlyLeuThrPheGlyTyrGluLeuAlaVa 28
880438 GCCGGAGTGTGTCTGCTGCCCTCGGTGATGGCAGCATGTGCGACGTCACTCCCT 880389
28 lileSerGlyAlaLeuLeuProLeuGlnLeuAspPheGlyLeuSerCysAl 45
880388 GGTACAGGTGCGCAACGACGACCTTCGTTGCCGATTTCCGGG..... 880349
45 euGluGlnGluPheLeuValGlySerLeuLeuGlyAlaLeuAla 61
880348 ..TCCACCCAGGCGCTGCTGGCTGACCATCACCGCTACATGCTCGCG 880301
62 SerLeu.....ValGlyGlyPheLeuIleAspCysTyrGlyAr 74
880300 TTGGCCACTGTGATCCCGACAGCGGTGGGGCGCGCGGTTCGGCAC 880251
74 glysGlnAlaIleLeuGlySerAsnLeuValLeuLeuAlaGlySerLeuT 91
880250 CAGCGCGCTTTTCATGGTTCGCTATTGGCTTACCCCTCGGCTCACCTGC 880201
91 hrLeuGlyLeuAlaGlySerLeuAlaTrpLeuValLeuGlyArgAlaVal 107
880200 TGTGGCAGTAGCACCAACATCTTCTGCTCATCATATTTGCTGTGTGTC 880151
108 ValGlyPheAlaIleSerLeuSerSerMetAlaCysCysIleTyrValSe 124
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Percent Similarity: 45.124 Percent Identity: 25.473

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 US-09-652-292-2 x US-08-676-967-5/rev ..

Align seg 1/1 to reverse of: US-08-676-967-5 from: 1 to: 2277

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7 ValLeuProLeuCys...AlaSerValSerLeuLeuGlyGlyLeuThrPh 22
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2118 CTGCTTCCACTGTTGATCTCGGGCTTGGGCTTCTTGGG.....GTGCA 2075

22 eGlyTyRGlulLeuAlaValIleSerGlyAlaLeuLeuProLeuGlnLeuA 39
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39 spPheGlyLeuSerCysLeuGlnGln...GluPheLeuValGlySerLeu 54
||:||||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
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55 LeuLeuGlyAlaLeu..... 59

1992 GCGCTGGGCGAGCTCCACCTGCTCCACCTCGGCTTGGTCTGGAAGCCGG 1943

60 .....LeuAlaSerLeuValGlyGlyPheLeuIleA 70

1942 TCCAGCTGGTGGCTGGCGGCTTGGCTTGTCTGGGGGGGACCTTGGCTC 1893

70 spCysTyRGlYArgLysGlnAlaIleLeuGlySerAsnLeuValLeuLeu 86
||| ::::::::::::::
1892 TGCTCTCCGT.....GTGGTCTGGGCGGCTTCTGTGCTGGTGC 1852

87 AlaGlySerLeu.....ThrLeuGlyLeuAla...GlySerLeuAl 99
|||:||||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
1851 CTTGGGGGCTCGGGCTGGGCTTCTGGGCTGGGCTGGGCTGGGCTTGC 1802

99 aTrpLeuValLeuGlyArgAlaValValGlyPheAlaIleSerLeuSerS 116
|:||||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
1801 TGGCATCTTCTCAGCTCGCTGGTGGATGGCGAGCTCTTCATCTTCAGC 1752

116 erMetAlaCysCys.....IleTyRValSerGluLeuValGlyPro 129
||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
1751 TTGGGGGGTCTCCAGGCTGAACCTCCAGCATGGGGCTTCAGGGGGCC 1702

130 ArgGlnArgGlyValLeuValSerLeuTyRGlulA...GlyIleTh 144
|||:||||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
1701 GAAGATCTCGGGTGTGTGTGTATAGGCGCAGGCGCTTCAGGGCGTGT 1652

144 rVal.....GlyIleLeuLeuSerTyRAlaLeuAsnT 155
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1651 CGTCTCTGGAACCTGGGGAAGGCTAGCCAGGCTCTGGCCCTTCATG 1602

155 yRAlaLeuAlaGlyThrProTrpGlyTrpArgHisMetPheGlyTrpAla 171
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1601 TTGGCGTGCAGCCCTTCAGTTCGG.....CATCAGCGGCACTCCTT 1558

172 ThrAlaProAlaValLeu.....GlnSerLeuSerLe 182
||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
1557 GATGCGGACCGCTTCTCGCGCTGGTGGCGCTCAGCAGCAGCTTGC 1508

182 uLeuPheLeuProAlaGlyThrAspGluThr.....A 193
|||:||||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
1507 GCTGCTTGTCTCAGCGCTTGGGAGGTTGTGCAGGCAACAGCGGGTG 1458

193 laThrHisLysAsp.....LeuIleProLeuGlnGly 204
|||:||||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
1457 CGGCTCAGGAGATGTTCTGGTCTTCACTTGTGGTGTTCAGCAGCTC 1408

205 GluAlaProLysLeuGlyProGlyArgProArgTyRSerPheLeuAspLe 221
|||:||||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
1407 GAAGCGCTCGCGCTTGGCCATGTCGGGCGGCTCAGCGCTCGCGGCT 1358

221 uPheArgAlaArgAsn...MetArgGlyArgThrVal..... 234
|:||||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|

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1357 TGGTGGCGGGGGATCAGCCCTCGCGGGCCAGGTACAGGTTCGGGGTG 1308

235 ....GlyLeu.....GlyLeuValLeuPheGlnLeuThr 245
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1307 CCGGTGGGCTTCTTCACTTGGTGTCTCAGCTTGGCGGCTTCGTCGG 1258

246 GlyGlnProAsnVal.....LeuCysTyRAl 254
|||:||||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
1257 GGTCAAGGCGAGTCCACCTTCACTTGGCGGCTCCAGCTTCAGGCGC 1208

254 aSerThrIlePheSerSer.....V 261
|||:||||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
1207 CGGCTCTGTTCTCGGGCTGGCGGCGCAGGAGCTTCTGGGCGGCTCC 1158

261 aGlyPheHisGlyGlySerSerAlaValLeuAlaSerValGlyLeuGly 277
|||:||||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
1157 TGGGTATGAACCTGGGAAGGCGCAGCTTGTCTGTCTGGTGTTCGGG 1108

278 AlaValLysValAlaAlaThrLeuThr..... 286
::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
1107 GTGACAGCATGCGCAGCTACTTCACTTGGCGGAACTGCTGCAGCAGCT 1058

287 .....A 287

1057 CGCCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1008

287 laMetGlyLeuValAspArgAlaGlyArgAlaLeuLeu..... 301
::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
1007 GTCTTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 958

302 .....AlaGlyCysAlaLeu... 306
|||:||||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
957 CACCTGCAGCGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 908

307 .....MetAlaLeuSerValSerGlyIleGlyLeuValSerPheAlaValP 322
|||:||||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
907 CCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 859

322 roMetAspSerGlyProSerCysLeuAlaValProAsnAlaThrGlyGln 338
|||:||||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
858 .....CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 829

339 ThrGly.....LeuProGlyAspSerGlyLe 347
|||:||||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
828 GCGGGGCGGCTTCAAGCGGCTTCTGGATCTGCAGGCTTGGTCACTCT 779

347 uLeuGlnAspSerSerLeuProProIleProArgThrAsnGluAspGlnA 364
|||:||||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
778 TGCTCTCGATGT.TCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 733

364 rgGluProIleLeuSerThrAlaLysLysThrLysProHisProArgSer 380
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381 GlyAspProSerAlaProProArgLeuAlaLeuSerSerAlaLeuProGl 397
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688 ..CCTCCATGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 642

397 yProProLeuProAlaArgHisAlaLeuLeuArgTrpThrAlaLeu 413
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641 T.....GCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 598

414 LeuCysLeuMetValPheValSerAlaPheSerPheGlyPheProVa 430
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597 CTGGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 560

430 l.TrpTrpLeuVal..... 434
|||:||||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
559 CCAGCGGCGGCTGCGGCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 510

435 .....LeuSerGl 437
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[illegible]

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seq_documentation_block:
; Sequence 5, Application US/08676974
; Patent No. 5770422
; GENERAL INFORMATION:
; APPLICANT: COLLINS, KATHLEEN
; TITLE OF INVENTION: Human Telomerase
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: Science & Technology Law Group
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/676,974
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman Ph.D., Richard A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UCB96-055
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415)343-4342
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2277 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-676-974-5

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alignment_scores:	
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Ratio: 0.540                      Gaps: 36
Percent Similarity: 45.124      Percent Identity: 25.473

alignment_block:
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39  spPheGlyLeuSerCysLeuGluGln...GluPheLeuValGlySerLeu 54
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2042 ATCTGGGGCGCGGTGGCTGGCAGGGCCAGCACCTTGGCGGCTTCTT 1993
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55  LeuLeuGlyAlaLeu.....
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1992 GCGCTCGGCGAGCTCCACCTGTCTCCACCTCGGCTTGGTCTGGAAGCCGG 1943
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155  yrAlaLeuAlaGlyThrProTyrGlyTyrArgHisMetPheGlyTyrAla 171
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205  GluAlaProLysLeuGlyProGlyArgProArgTyrSerPheLeuAspLe 221
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235 ....GlyLeu.....GlyLeuValLeuPheGlnLeuThr 245
1307 CCGGTGGGCTTCTACCTTGGTGTCTGCAGCTTGGCGGCTCTCGCG 1258
246 GlyGlnProAsnVal.....LeuCysTyrAl 254
1257 GGTACGGCCAGGTCCACCTTCAGCTGGCGGCGCTCCAGCTTCAGGCCG 1208
254 aSerThrIlePheSerSer.....V 261
1207 CGGCTCGTTCGGGGCTGGCGGCCAGCAGCACTTCTGGCGGCTCC 1158
261 aGlyPheHisGlySerSerAlaValAlaLeuValGlyLeuGly 277
1157 TGGGTGCATCACTGGCGGAAGCGCAGCCCTTGTCTGTCTCGTGTGG 1108
278 AlaValLysValAlaAlaThrLeuThr..... 286
1107 GTGCAGCAGCATCGGCACGTACTTCAGCTCGCGCACTGCTGCAGCAGCT 1058
287 .....A 287
1057 CGCCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1008
287 laMetGlyLeuValAspArgAlaGlyArgAlaLeuLeuLeu..... 301
1007 GTCTTGGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 958
302 .....AlaGlyCysAlaLeu... 306
957 CACCTGCAGCGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTGG 908
307 ....MetAlaLeuSerValSerGlyIleGlyLeuValSerPheAlaValP 322
907 CCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 859
322 roMetAspSerGlyProSerCysLeuAlaValProAsnAlaThrGlyGln 338
858 .....CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 829
339 ThrGly.....LeuProGlyAspSerGlyLe 347
828 GCGGGGCGCTTACAGCGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 779
347 uLeuGlnAspSerSerLeuProProleProArgThrAsnGluAspGlnA 364
778 TGTCTCTGATGT..TCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 733
364 rgGluProIleLeuSerThrAlaLysLysThrLysProHisProArgSer 380
732 GTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 689
381 GlyAspProSerAlaProProArgLeuAlaLeuSerSerAlaLeuProGl 397
688 ...CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 642
397 yProProLeuProAlaArgGlyHisAlaLeuLeuArgTTPThrAla..Leu 413
641 T.....GCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 598
414 LeuCysLeuMetValPheValSerAlaPheSerPheGlyPheProVa 430
597 CTGGGTGCTCTGTACTTGTCT.....CTTGGCCAGGCCAGCT 560
430 l..ThrTrpLeuVal..... 434
559 CCAGGCCACGGTGGCGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 510
435 .....LeuSerGly 437
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seq\_name: /cgn2\_6/ptodata/2/lna/5B\_COMB.seq:US-09-098-487-5

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seq_documentation_block:
; Sequence 5, Application US/09098487
; Patent No. 5917025
; GENERAL INFORMATION:
; APPLICANT: COLLINS, Kathleen
; TITLE OF INVENTION: Human Telomerase
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Science & Technology Law Group
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/098.487
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman Ph.D., Richard A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UCB96-055
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415)343-4342
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2277 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-098-487-5
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alignment\_scores:

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Quality: 157.50          Length: 687
Ratio: 0.540            Gaps: 36
Percent Similarity: 45.124  Percent Identity: 25.473

alignment_block:
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Align seg 1/1 to reverse of: US-09-098-487-5 from: 1 to: 2277

7 ValLeuProLeuCys...AlaSerValSerLeuLeuGlyGlyLeuThrPh 22
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2118 CTGCTCCACTGGTGTGATCTGGGCTTGGGCTTCTGGG.....GTGCA 2075
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22 eGlyTyrCluLeuAlaValIleSerGlyAlaLeuLeuProLeuGlnLeuA 39
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39 spPheGlyLeuSerCysLeuGluGln...GluPheLeuValGlySerLeu 54
|||||
2042 ATCTTGGGCGCGGTGCTGGCGAGGCCAGACCTTGGCGGCTTCTT 1993
|||||

55 LeuLeuGlyAlaLeu..... 59
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1992 GCCCTCGGCAGCTCCACCTGCTCCACCTCGGCTTGGTCTGCAAGCCG 1943
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60 .....LeuAlaSerLeuValGlyGlyPheLeuIleA 70
|||||

1942 TCCAGCTGGTGTCTGCGGGCTTTCGCTTCGGGGGCACCTTGTCTC 1893
|||||

70 spCysTyrGlyArgLysGlnAlaIleLeuGlySerAsnLeuValLeuLeu 86
|||||
1892 TGTCTCTCGT.....GTGGTCTGGGGCGCTTCTGTCTGTGCTC 1852
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87 AlaGlySerLeu.....ThrLeuGlyLeuAla...GlySerLeuAl 99
|||||
1851 CTTGGCGGCTCGGGCTGCCCTTCTGGGCTCGCGGTGGCGGCTTCG 1802
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99 atTrpLeuValLeuGlyArgAlaValGlyPheAlaIleSerLeuSerS 116
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116 erMetaAlaCysCys.....IleTyrValSerGluLeuValGlyPro 129
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130 ArgGlnArgGlyValLeuValSerLeuTyrGluAla.....GlyIleTh 144
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144 rVal.....GlyIleLeuSerTyrAlaLeuAsnT 155
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193 laThrHisLysAsp.....LeuIleProLeuGlnGly 204
|||||
1457 CGGCTCACAAGATGTTCTGCTCTTCAGCTTCTGGTGTCTTCAGCAGCTC 1408
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205 GluAlaProLysLeuGlyProGlyArgProArgTyrSerPheLeuAspLe 221
|||||
1407 GAAGCGCTCGCGCTTGGCATGTGCGGGCGGCTCATCGGCTTCGGCGGCTC 1358
|||||

```

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509 GCCTTGGCGGCTCCAGCAGGTTCTTGNACTGCAGGAAGCCGAGACCCGGC 460
      ::
437 uIleTyrProValGlulIleArgGlyArgAlaPheAlaPheCysAsnSerP 454
      :||| ||| ::||| ||| ::||| ::|||
459 CATCTTGGCGTGGCTTGGGGG...ATCTTCACCTCCAGCAGCGGCGC 413
      :||| ||| ::||| ||| ::||| ::|||
454 heAsnTrpAlaAlaAsnLeuPheIleSerLeuSerPhe..... 466
      ||||| ||| ::||| ||| |||||
412 CGAACTGGGCAACACGGCTTTCAGGTCGTCCTCGCTGCACCTGAAGCTC 363
      :||| ||| ::||| ||| |||||
467 ..LeuAspLeuIleGlyThrIleGlyLeuSerTrpThrPheLeuLeuTy 482
      ||| ::||| ||||| ||||| ::|||
362 AGGTTCGGATGATCAGCGCGGCTCTCTTCGCGCACCTTGGCCTTCTT 313
      :||| ||| ::||| ||| ::|||
482 rGlyLeuThrAlaValLeuGlyLeuGlyPheIleTyrLeuPheValProG 499
      :||| ::||| ::||| ||||| ::|||
312 GGCCTTGGCTCCCTTCCTGGGGCACTCG...CTGTCTCTGTTCTTGGCC 266
      :||| ||| ::||| ||| ::|||
499 luThr.....LysGlyGlnSerLeuAlaGluIleAspGlnGln 511
      ::||| ::||| ||||| ::|||
265 TCTCCTTGGTCTTGTGGCGAGCTTCTTCTTGGCGCAGGTCAGGTTGATC 216
      :||| ||| ::||| ||| ::|||
512 PheGlnLysArgArgPheThrLeuSerPheGlyHisArgGlnAsnSerTh 528
      :||| ||| ::||| ||||| |||||
215 TTGCAGCCCTCGAAGGTGGTGATCTCTTCAGGGGGCGCTGCACGCTCTC 166
      :||| ||| ::||| ||| ::|||
528 rGlyIle 530
      :||| ||| ::||| ||| ::|||
165 CAGCATG 159
      :||| ||| ::||| ||| ::|||

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